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OM nucleic - protein search, using frame_plus.n2p model

Run on: August 22, 2003, 13:49:06 ; Search time 30 Seconds
(without alignments)
4380.584 Million cell updates/sec

Title: US-09-745-506-74
Perfect score: 2789
Sequence: 1 GCGATTGTTATCTGTGCT.....TCGTGTTACTTAACATTCAA 1553

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 328717 seqs, 42310858 residues
Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=framer.n2p.model -DEV=x1p
-O=/cgn2.1/uspro.spool/US09745506/runat_22082003_132711_10806/app_query.fasta.1.1735
-DB=Issued_Patents_AA -OPMT=fastan -SUFFIX=n2p.ra1 -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=human4.0.cd1
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPM=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09745506.ecgn.1.1.38.0runat.22082003.132711.10806 -NCP=6 -ICPU=3
-NO_MAP -LARGEQUERY -NIG_SCORES=0 -WAIT -DSRBLCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FgapEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: Issued_Patents_AA:*
2: /cgn2.6/ptodata/1/1aa/5a_COMB.pep:*
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6: /cgn2.6/ptodata/1/1aa/5a_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	321.5	11.5	378	4	US-09-107-532A-4742
2	305	10.9	367	4	US-09-134-001C-3678
3	106	3.8	256	4	US-09-252-991A-24651
4	104.5	3.7	473	4	US-09-328-352-4482
5	103.5	3.7	262	4	US-09-146-053-2
6	103	3.5	673	4	US-09-146-053-2
7	97.5	3.5	509	4	US-09-252-991A-28680
8	97	3.5	588	4	US-09-328-352-7994
9	96.5	3.5	493	4	US-10-002-593-10
10	96	3.4	503	3	US-08-911-853-7
11	96	3.4	503	3	US-09-479-409-7
12	96	3.4	503	4	US-09-479-453-7

C	13	96	3.5	724	4	US-09-984-890-2	Sequence 2, Appl1
	14	95	3.4	638	2	US-08-681-151-3	Sequence 3, Appl1
	15	95	3.4	804	4	US-09-134-001C-5218	Sequence 5218, Ap
	16	95	3.4	1172	1	US-08-313-2888-19	Sequence 19, Appl
	17	94.5	3.4	251	4	US-09-198-452A-156	Sequence 156, Appl
	C	18	93.5	488	4	US-09-252-991A-31307	Sequence 31307, A
	C	19	93	787	4	US-09-252-991A-28939	Sequence 28939, A
	C	20	92	2930	4	US-09-417-822-2	Sequence 2, Appl1
	C	21	91	501	2	US-08-969-630-4	Sequence 4, Appl1
	C	22	91	735	4	US-09-134-001C-3440	Sequence 3440, Ap
	C	23	90.5	417	4	US-09-252-991A-23413	Sequence 23413, A
	C	24	90.5	1537	4	US-09-376-330-2	Sequence 2, Appl1
	C	25	90	281	4	US-09-252-991A-25970	Sequence 25970, A
	C	26	90	32	4	US-09-328-352-4432	Sequence 4432, Ap
		27	90	1058	4	US-09-328-352-4276	Sequence 4276, Ap
		28	89.5	1651	3	US-09-340-245A-18	Sequence 18, Appl
		29	89.5	2512	2	US-08-801-263A-9	Sequence 9, Appl1
		30	89.5	2512	3	US-09-102-248-9	Sequence 9, Appl1
		31	89.5	2512	4	US-09-367-76A-9	Sequence 9, Appl1
		32	89	907	4	US-09-170-496D-264	Sequence 264, Appl
		33	89	907	4	US-09-170-496D-278	Sequence 278, Appl
		34	89	951	4	US-09-328-352-4456	Sequence 4456, Appl
		35	88.5	405	2	US-08-222-719-2	Sequence 2, Appl1
		36	88.5	405	2	US-08-470-925-2	Sequence 2, Appl1
		37	88.5	405	2	US-08-471-613-2	Sequence 2, Appl1
		38	88.5	405	5	PCT-US93-10443-2	Sequence 2, Appl1
		39	88.5	498	4	US-08-702-598-2	Sequence 2, Appl1
		40	88.5	514	4	US-09-328-352-6997	Sequence 6997, Ap
		41	88.5	800	3	US-08-776-263-3	Sequence 3, Appl1
		42	88	1154	4	US-09-134-001C-3428	Sequence 3428, Appl
		43	87.5	355	4	US-09-134-001C-5391	Sequence 5391, Appl
		44	87.5	498	3	US-09-134-607A-19	Sequence 19, Appl
		45	87.5	609	3	US-08-927-219-129	Sequence 129, Appl

ALIGNMENTS

RESULT 1
US-09-107-532A-4742
Sequence 4742, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arieliello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277

```

; INFORMATION FOR SEQ ID NO: 4742:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 378 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYDROPHILIC: YES
;   ORIGINAL SOURCE:
;       ORGANISM: Enterococcus faecium
;   FEATURE:
;       NAME/KEY: misc.feature
;       LOCATION: (8) LOCATION 1...378
;   SEQUENCE DESCRIPTION: SEQ ID NO: 4742:
US-09-107-532A-4742

Alignment Scores:
Pred. No.:      3,19e-25      Length:      378
Score:          321.50        Matches:      103
Percent Similarity: 45.19%    Conservative: 80
Best Local Similarity: 25.43%  Mismatches:   133
Query Match:    11.53%       Indels:       89
DB:              4           Gaps:          17

US-09-745-506-74 (1-1553) x US-09-107-532A-4742 (1-378)

OY      230 TCTTCCGCTTCCTTCATGATGATGAAAGGCTCTCTTCTTCTTCCTGATGACTTTCATCC 289
DB      9  SerGlyArgThrPhe-----IleGlnLysPheGluSerTyrCysPro 22
OY      290 CTCGCTTTGGTGGAGTTGGACAAATGTGGATTA-----CTGTGGAACA 337
DB      23  GlnTrpLeuAlaGluGlnGlyAspProValGlyLeuHisIleGlyThrLeuAspLysPro 42
OY      338 AGCCACACCATCTGTAATAATCACTCTTCTGACCAATGACTGACTGAGAAAGTGTATG 397
DB      43  -----IleGlnArgValIleMetThrLeuAspValArgProGluVal 57
OY      398 GAGGAGTGTCTGCAAAAAGAGCAGACCTCATTTCTCTTACCATCCGCTATCTCCGA 457
DB      58  GlnGluAlaIleLysLysLysIleAspLeuLeuIleAlaLysHisProProlIlePheArg 77
OY      458 CCCATGAGCCGATACCTGGAACACATGAGAGCGCCGTGGATCCGGCTGTGGAG 517
DB      78  ProValLysArgLeuValThrAspGlnProGlnGlnLysMetTyrAlaAspLeuLys 97
OY      518 AACAGAGTGGTATCTACTCTCTCATACAGCCTATGATGCTGCCGCCAGGGCGCTCAAC 577
DB      98  HisAspIleAlaValTyrAlaIleHisThrAsnMetAspIleIleTrpAspLysLeuAsn 117
OY      578 AACTGGTGGGCTAAAGGCTTGA-----GCTTGACCTCCAGGCC 619
DB      118  AspTrpPheCysGluLeuLeuGlyIleGluValGluSerTyrLeuValLysThrHisGlu 137
OY      620 ATACATCTTCCAAAGCTCCCAACTACACTACAGAGGAAACACCGAGTAGAATTAAC 679
DB      138  IleHisTyrLysLysLeuAlaValTyr-----ValPro 148
OY      680 GTTAATCACTACCCCAAGACCTGGACAAAGTCATGCTGCAAGTGAAGA----- 727
DB      149  ValAspHisAlaGlnLysMetArgGluValLeuAlaIleAlaGlyAlaGlyThrGlnGly 168
OY      728 ---ATTGACGGTGTCTGCTCACTCTTTCT----- 757
DB      169  AspTyrThrGlnGlyThrSerPheThrSerIleGlyHisGlyArgPheThrProGluAlaGly 188
OY      758 -----GTTAGACCTGTAATGAGCAACAACGAGATTAATCTGAATTGT 802
DB      189  AlaGlnProAlaIleGlyLysValGlyLysThrGln----- 201
OY      803 ACTCAGAAAGCTTTGATCAGAGTGTGATTTCTTCCCGAACAAACATTTATCAG 862
DB      202  ValGlnGluAlaLysValGluValIleLeuProGluTrpIleGluLysGlnValIleGln 221

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OY      863 AAGACG-----GAATTTCTGTCACTGAGAG 889
DB      222  AlameTarSerAlaHisProTyrGluGlnProAlaTyrAspLeuPheAlaIleAspL 241
OY      890 CCTTGGCTTCTACATCTGGAATGGAGCGTTATGCAACATGATGATCTGTCTCCGT 949
DB      242  ProValGluMetPhe--GlyLeuGlyArgValGlyGluLeuProGlnGlnIlePheIle 260
OY      950  GCAACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1009
DB      261  GluAlaPheValGluGlnValLysGlnLysAlaPheGlnLeuAspArgLysAlaIleVal 279
OY      1010  GGGGTGGGAGACCTTGAAGTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1069
DB      280  --GlnProLysAsnAlaLysSerSerValLysArgIleAlaIleCysGlyGlySerGly 298
OY      1070  AGCAGCGTTG---CAGCGGTG-----GAGCGTGCCTTTCCTTCACAGGAGAGATG 1120
DB      299  GluLysPheTyrProGlnAlaIleAlaGlnArgAlaAspValTyrIleThrGlyAspIle 318
OY      1121  TCCCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1168
DB      319  TyrTyrHisThrAlaHisAspMetGlnSerAlaGlyLeuIleAlaIleAspProGlyHis 338
OY      1169  -----CTGTGGAACAACAGCAACCTGACGAGCTTTCTTCTGACCTTCA 1216
DB      339  TyrIleGluSerLeuCysLysGlnArgPheIleGlnLys---PheGluSerTrpLysGln 357
OY      1217  GATATGCTGATTCATCTCACTTGGAGAT---AAGATTAATTAATTAATTAATTAATTA 1273
DB      358  Glu-----GlnAsnTrpAspIleAsnPheValSerGluTrpAsn 371
OY      1274  AGGACCTCTTCAAG 1288
DB      372  ThrAsnProPheGln 376

RESULT 2
US-09-134-001C-3678
; Sequence 3678, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;   APPLICANT: Lynn Doucette-Stamm et al
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
;   TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: GTC-007
;   CURRENT FILING DATE: 1998-08-13
;   PRIOR APPLICATION NUMBER: US 60/064,964
;   PRIOR FILING DATE: 1997-11-08
;   PRIOR APPLICATION NUMBER: US 60/055,779
;   PRIOR FILING DATE: 1997-08-14
;   NUMBER OF SEQ ID NOS: 5674
;   SEQ ID NO 3678
;   LENGTH: 367
;   TYPE: PRT
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3678

Alignment Scores:
Pred. No.:      1.77e-23      Length:      367
Score:          305.00        Matches:      96
Percent Similarity: 43.54%    Conservative: 76
Best Local Similarity: 24.30%  Mismatches:   145
Query Match:    10.94%       Indels:       78
DB:              4           Gaps:          13

US-09-745-506-74 (1-1553) x US-09-134-001C-3678 (1-367)

OY      245  ATGATTTGAAGGCTCTCTCTTCTCTGATGATGATGATGATGATGATGATGATGAT 304
DB      2  MetLysIleSerGluLeuMetGlnValLeuAsnHisValProPheHisGlnAlaGlu 21
OY      305  AGTTGGACATGTGTTGGATCTGCTGGAACCAACCCACACATCTGTAATTAATCACTC 364

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OY	848	AAACAACTTATTCAGAGAGACGGAAATTCCTGCACTGGAGAGCCCTTGGCTTCATCACT	907
	158	ArgspAlaLeuGlyArg-----GluProLeuValAspAla	170
OY	908	GGAAATGGACGGTATGCAACACTGATGAATCTGTCCCTGGCAACCATGATTGATCGA	967
	171	Gly-----	171
OY	968	ATAAAGACACSTAAAACSTATCTCATATTCGCTTAAGCCCTTGGGGTGGGAGAACSTTA	1027
	171	-----	171
OY	1028	GAGTCTCAAGTCAAAGTCGTGACCCCTGTGTGCTGGTGTGGAGACGGTCTTG--CAG	1084
	172	---GlnProIleArgAlaGlyIleAlaIleTProysThrGlyGlyAlaGlnGlyTyrIleAspIle	190
OY	1085	GGTGTGTGAGCST-----GACSTTATACCTCCACAGGTGATGATGCTCCATCATGATCACTTGG	1138
	191	AlaIleIleAlaIleArgValAspAlaIleTyrIleuThrGlyValAspGluGlnIleThrValHis	210
OY	1139	GATGCTGCTGCCACAGCAATATAATGTCACTCTGTGTGAACACAGCAACAGTGAACGAGCC	1196
	211	SerAlaArgGluAsnGlyIleSerThrIleLeuAlaIleAspGlnHisAlaIleThrGlyArgGly	230
OY	1199	TTTCTTCTGACCTTCGAGATATGCTG	1225
	231	GlyValGlnAlaLeuGlyAspTyrIleu	239

Alignment Scores:

Pred. No.:	0.285	Length:	588
Score:	97.00	Matches:	67
Percent Similarity:	38.61%	Conservative:	50
Best Local Similarity:	22.11%	Mismatches:	96
Query Match:	3.48%	Indels:	90
DB:	4	Gaps:	13

US-09-745-506-74 (1-1553) x US-09-328-352-7994 (1-588)

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OY 563 CCCGAGGCGGTGAACACTGTTGGCTTAAGGCGTTGACTCTCAGGCCANA 622
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 249 ProleuGlnleuAlaasnArgleuAlaSerArgleuValMetSerGlnMetaspIle 268
OY 623 CATCCTCCAAAGCTCC-----AACTACCCCTACAGAGGGAACCAACCGA 667
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 269 SerGlnLysArgValProGlnAspGlyArgIleLysleuLysLeuSerLysPala 288
OY 668 GTAGAATTCAAGCTTAACCTACACCCCAAGACCTG-----GACAAGTCATG 712
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 289 IleAspPheArgValAsnSerLeuProThrLeuPheGlyGlnLysLeuValIleuArgIle 308
OY 713 -----TCTGCACTGAAAGGAATTGACGGTGTCTGCTCATCTTTTCTGCT 760
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 309 LeuAspProSerSerAlaMetLeuGlyIleAspAlaLeu----- 321
OY 761 AGGACTGCTTAATGAGAAACAAACCGGATTAATCTGAATTTGCTCAGAAAGCTTGATG 820
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 322 -----GlyTyrGlnLysAsp-----GlnLysAlaLeuPhe 331
OY 821 CAGTGTGATGATTTCTTCCCGAACAACAATTATCAGAGACGAATTTCTGTCA 880
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 332 -----MetGlnAlaLeuAspLysProGlnGlyMetLeuLeuIleThrGlyProThrGly 349
OY 881 CTGAGAGACCTTTGCTTACATACTGGAATGGACGGTTATGACACTGATGATCTP 940
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 350 SerGlyLysThrValSerLeuTyrThrGlyLeuAsnIleLeuAsnThr-----GlnSer 367
OY 941 GTCCTCCCTGGCAACCTGATTCGATTCGAATRAAAGACCTAATA---CATCTCATATT 997
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 368 SerAsnIleSerThrIleGlnAspProValGlnIleAsnLeuGlnIleAsnGlnVal 387
OY 998 CGCTTAGCCCTGGGTGGGAGAACCTTAGAGCTCAAGTCAAAAGTCGGCCCTGTGT 1057
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 388 AsnValAsnProLysValGlyLeuThrPheAlaIleAlaLeuLys----- 402
OY 1058 GCTGCTTGTGGAGACGCTTCTGACGGGTGTGAGGCTTACCTTACCTCAGAGGTAG 1117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 403 -----SerPheLeuArg---GlnAspProAspIleIleMetValGlyGln 416
OY 1118 ATGTCCCATCATGATTACT-----TTGGATGCTGCTTCCCAAGTAATTAATGTC 1165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 417 IleArgAspLeuGlnThrIleGlnIleAlaIleLysAlaIleGlnThrGlnMetVal 436
OY 1166 ATCTCTCTGACACAGCAACTGACAGAGGCTTTCTTCTGACCTTCAGATATGCTG 1225
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 437 MetSerThrLeuHisThrAsnSerAlaProGlnThrLeuThrArgLeuAsnMet--- 455
OY 1226 GATTTCACTTGGAGATAAGATAAATTATTCCTATCAGAGACTGACAGGACCTCTT 1285
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 455 ----- 455
OY 1286 CAGGTGTATTAATTGAGAAACATCAGATACACATTCCTACAAATCAGTGTGATGCC 1345
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 456 -----GlyValPro 458
OY 1346 AACTTAATTTGTAACATGAGTCAAGTGGACCTGCTGCTTCAGAGAGTGTCTTGAGAG 1405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 459 SerPheAsnIle---AlaThrSerValAsnLeuValIleAlaGlnArgLysAlaArgArg 477
OY 1406 GTATTCATCA 1414
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 478 LeucYsSer 480

RESULT 9

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US-10-002-593-10
; Sequence 10, Application US/10002593
; Patent No. 6586198
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Brown, Nancy J.
; TITLE OF INVENTION: BIOLOGICAL MARKERS AND DIAGNOSTIC TESTS FOR ANGIOTENSIN CONVERTING ENZYME INHIBITOR AND VASOPRESSIN RECEPTOR INHIBITOR ASSOCIATED ANGIOEDEMA
; FILE REFERENCE: Atty Docket No. 6586198 1242/48/2
; CURRENT APPLICATION NUMBER: US/10/002,593
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/244,524
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-593-10

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Alignment Scores:

Pred. No.:	0.289	Length:	493
Score:	96.50	Matches:	60
Percent Similarity:	35.23%	Conservative:	45
Best Local Similarity:	20.13%	Mismatches:	108
Query Match:	3.46%	Indels:	85
DB:	4	Gaps:	12

US-09-745-506-74 (1-1553) x US-10-002-593-10 (1-493)

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OY 446 CCTATCTCCGACCATGAGCCGATTAACCTGGAACATGAGAGCCCTGTGATC 505
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 ProIleTyrAlaLeuGlnGlnAlaPheThrGlySerThrIleProGlnGlnLysValPro 40
OY 506 CGGGCTCTGGAGAAACAGAGTGTACTACTCCATACAGCTTATGATGCTGCGCC 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 41 -----SerGlyValArgSerGlnMetGlnLysGlnLysValPro 54
OY 566 CAGGCGGTC-----AACACTGTTGGCTTAAGGCTTGGAGCT 604
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 55 ThrAlaValLeuLeuSerAlaLeuGlnGlnThrAlaIleProLeuPheAsn----- 70
OY 605 TGTACTCCAGCCCATACATCTTCCAAAGCTCCCACTACCTCAGAGGGAACAC 664
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 71 -----LeuArgAlaSerAspIleProTyrAsnPro----- 80
OY 665 CGAGTAGAATTCAACGTTACTACACCCAGACCTGCAAAAGCATGCTGCGAGTGA 724
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81 -----PhePheTyrSerTyrThrLeuLeuThrAsp----- 90
OY 725 GGAATTGACGCTTCTTCTCATTCTTTTCTGCTGAGACTGTGTAATGAGAACAA 784
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 91 -----SerSerIleArgLeuPheAlaAsnLysSerArgPheSerSerGlnThrLeuSer 108
OY 785 CGGATTAATCTGATTTGATCTCAGAGAGCTTGTATGACAGGTGATGATTTT----- 835
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 109 TyrLeuAsnSerSerCysThrGlyProMetCysValGlnIleGlnAspTyrSerGlnVal 128
OY 836 -----CITTCCCGGACAAA 850
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 129 ArgAspSerIleGlnAlaTyrSerLeuGlyAspValArgIleThrPilleGlyThrSerTyr 148
OY 851 CAACTTAATCAGAAACGAAATTTCTGTCACGAGAGACCTTGTCTTACATATCTGGA 910
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 149 ThrMetTyrGlyIleTyrGlnMetIleProArgGlnLys----- 161
OY 911 ATGGAGCGTTATGACACATGATGAATTCGTCTCCCTGCAACCATGATGATGATA 970
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 162 -----LeuValThrAspThrTyrSerProValMetMetThrLysAlaVal 176

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QY 971 AAAAGACAC-----CTAAACTATCTCATATTCGCTTAGCCCTTGCGGTG 1015
Db 177 LysAsnSerIysGlnGlnAlaLeuLeuYAlaSerHisValArgAspAlaValAlaVal 196
QY 1016 GGGAGA-----ACCTTAGAGTCGCAAGTCGCAAGTGGCCCTGTGTGCTTCT 1066
Db 197 ILAATgTyrLeuValTyrLeuGlnLysAsnValProLysGlnTyrValAspGlnPheSer 216
QY 1067 GGGAGACGCTTCGACAGGTGTGAGCTTACCTTACCTACAGAGGTGAGTGGCAT 1126
Db 217 G1A1AlaLeuValAlaValAspIysPheArgGlyGlnGlnInPheSerSerGlyProSer 235
QY 1127 CATGATACCTTGGATGCTGCTTCCCAAGATTAATGTCATCTGTGAACACAGCAAC 1186
Db 236 PheGlnThrIleSerAlaSer-----GlyLeuAsnAlaAlaLeuAlaHisTyrSerPro 253
QY 1187 ACAGAA-----CGAGGCTTCTTTCGACCTTGACATATGCTGAGTCT 1231
Db 254 ThrIysGlnLeuAsnArgLysLeuSerSerAspIleuMetTyrLeuLeuAspSer 271

RESULT 10

US-08-911-853-7
Sequence 7, Application US/08911853
Patent No. 6048710

GENERAL INFORMATION:

APPLICANT: Gerritse, Gijbert
APPLICANT: Quax, Wilhelmus J.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,853
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/699,092
ATTORNEY/AGENT INFORMATION:
NAME: Gjalster, Debra J
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC361-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-911-853-7

Alignment Scores:

Pred. No.: 0.331 Length: 503
Score: 96.00 Matches: 62
Percent Similarity: 38.33% Conservative: 30
Best Local Similarity: 25.83% Mismatches: 61
Query Match: 3.44% Indels: 87
DB: 3 Gaps: 15

US-09-745-506-74 (1-1553) x US-08-911-853-7 (1-503)

QY 878 TCAGTGAGAAAGCT-----TTGCTTCTA-----CATAGTGGATGGAGGTTA 922
Db 252 AsnLeuArgIysProHisGlyIleIleLeuValThrGlyProHisGlySerGlyLysThr 271
QY 923 TGCACACTG-----GATGAATCTGTCTCCCGCAACCATG 958
Db 272 ThrThrLeuTyrAlaGlyLeuValThrLeuAsnSrpArgSerArgAsnIleLeuThrVal 291
QY 959 ATTGATGAATTAAGAACACCTTAACATATCTCATATTCGCTTAGCCCTTGCGGTGCGG 1018
Db 292 GlnAspProIleGlnTyrTyrLeuGln-----GlyIleGly 303
QY 1019 AGAACCTTAGAGTCTCAAGTCAAGTC-----GTGGCCCTGTGTGCTGGTGTGCGAGCAGC 1075
Db 304 GlnThr-----GlnValAsnProArgValAspMetThrPheAlaArgGlyLeuArg 320
QY 1076 GTTCTGACGGGTGTGAGAGTGCACCTTACCTTACCTACAGAGTGCATCATGATACT 1135
Db 321 AlaIleLeuArgGlnAspProAspValAlaMetValGlyGlnIleArgAspGlnGluThr 340
QY 1136 TTGGATGCTGCTCCAA-----GGAATTAATGTCATCTGTGAACACAGC 1183
Db 341 AlaAspIleAlaValGlnAlaSerLeuThrGlyHisLeuValLeuSerThrLeuHisThr 360
QY 1184 AACACTGACGAGGCTTCTTTCGACCTTGAGATATG-----CTG 1225
Db 361 AsnSerAlaValGlyAlaValThrArgLeuValAspMetGlyValGlnProPheLeuLeu 380
QY 1226 GATCTCAGCTGGAGATTAATGATTAATTTATCTATCAGAGACTGACAGGAGCCCTTT 1285
Db 381 SerSerSerLeu-----LeuGlyValLeuAla-GlnArgLeuValArgValLeu- 396
QY 1286 CAGGTGTATATATGACAGAAACATCAGATACA----- 1319
Db 397 ---CysValHisCysArgGlnAlaArgProAlaAspAlaIaGluCysGlyLeuLeuG1 415
QY 1320 -----CATGCC-----TACAATACAGCTGAGTGCACCACTTAATTTG 1357
Db 415 YLeuAspProHisSerGlnProLeuIleTyrHisAlaLysGlyCysPro 431
QY 1358 TAACATGAGTCAGTGGAGCTGTGTCTTCAGAGAGTGTCTTCGAGGGTATCATCATTT 1417
Db 432 -----GluCys----- 433
QY 1418 CCGGTTGTATATCTTATTCACCAATGTCTATGTGCTCGTAAGCTAATCTATATA 1475
Db 434 -----HisGlnGlnGlyTyrArg-----GlyArgGlnGlyIle 444

RESULT 11

US-09-479-409-7
Sequence 7, Application US/09479409
Patent No. 6225106

GENERAL INFORMATION:

APPLICANT: Gerritse, Gijbert
APPLICANT: Quax, Wilhelmus J.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/479,409

FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/911,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC361-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-479-409-7

Alignment Scores:
Pred. No.: 0.331 Length: 503
Score: 96.00 Matches: 62
Percent Similarity: 38.33% Conservative: 30
Best Local Similarity: 25.83% Mismatches: 61
Query Match: 3.44% Indels: 87
Gaps: 15

US-09-745-506-74 (1-1553) x US-09-479-409-7 (1-503)

```
QY 878 TCACGTGAGAGCCT-----TTGCTTCTA-----CATACTGGAATGGACGGTTA 922
Db 252 AsnLeuArgLysProHisGlyLeuValThrGlyProThrGlySerGlyLysThr 271
QY 923 TGCACACG-----GATGAATCTCTCCCGCCGACACCATG 958
Db 272 ThrThrLeuArgLysLeuValThrLeuAsnAspArgSerArgAsnIleLeuThrVal 291
QY 959 ATTGATCGAATAAAGACACCTAAACATATCTCATATTCGCTTACCCCTGGGGTGGG 1018
Db 292 GluAspProIleGluTyrLeuGlu-----GlyIleGly 303
QY 1019 AGAAGCTTGAAGTCTCAAGTCAAGTC---GTGGCCCTGTGCTGCTTGGGACAGC 1075
Db 304 GluThr-----GlnValAsnProArgValAspMetThrPheAlaArgGlyLeuArg 320
QY 1076 GTTCTGACAGGCTGTGAGGCTGACCTTACCTCAGAGTGACGATGCCATCATGACT 1135
Db 321 AlaIleLeuArgGlnAspProAspValValMetValGlyGluIleArgAspGlnGluThr 340
QY 1136 TTGGATGCTGCTCCCA-----GGAATTAATGTCACTCTGTGAACACAGC 1183
Db 341 AlaAspIleAlaValGlnAlaSerLeuThrGlyHisIleValIleuSerThrLeuHisThr 360
QY 1184 AACACTGAACGAGGCTTCTTCTGACCTTGCAGATATG-----CTG 1225
Db 361 AsnSerAlaValGlyAlaValThrArgLeuValAspMetGlyValGluProPheLeuThr 380
QY 1226 GATTCACACTGGAGAGTAAGATAATATATATCTTACAGAGCTGACAGGACCTCTT 1285
Db 381 SerSerSerLeu-----LeuGlyValLeuAla-GlnArgLeuValArgValLeu-- 396
QY 1286 CAGGTGATTAATGGAGAAACATCAGAGTAACA----- 1319
Db 397 -----CysValHisCysArgGlnAlaArgProAlaAspAlaAlaGluCysGlyLeuGlu 415
QY 1320 -----CATTC-----TACAATCAGCTGAGTGGCCAACTTAATTTG 1357
Db 415 yLeuAspProHisSerGlnProIleuLeuTyrHisAlaValGlyCysPro----- 431
QY 1358 TAAACATGAGTCACTGGGACTGTGTGCTTCCAGAGACTGCTTCCAGAGGTATCATCTT 1417
Db 432 -----GluCys----- 433
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QY 1418 CCGGTTGTATCTTATTCACCAAGTGTCTACGCTGCTGAAGTAAACTGTATA 1475
Db 434 -----HisGlnGlnGlyTyrArg-----GlyArgThrGlyIle 444

RESULT 12
US-09-479-453-7
Sequence 7, Application US/09479453
Patent No. 6313283
GENERAL INFORMATION:

APPLICANT: Gerritse, Gijbert
APPLICANT: Quax, Wilhelms J.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA

ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/479,453

FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/911,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC361-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
TELEFAX: 650-845-6504

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-479-453-7

Alignment Scores:
Pred. No.: 0.331 Length: 503
Score: 96.00 Matches: 62
Percent Similarity: 38.33% Conservative: 30
Best Local Similarity: 25.83% Mismatches: 61
Query Match: 3.44% Indels: 87
Gaps: 15

US-09-745-506-74 (1-1553) x US-09-479-453-7 (1-503)

```
QY 878 TCACGTGAGAGCCT-----TTGCTTCTA-----CATACTGGAATGGACGGTTA 922
Db 252 AsnLeuArgLysProHisGlyLeuValThrGlyProThrGlySerGlyLysThr 271
QY 923 TGCACACG-----GATGAATCTCTCCCGCCGACACCATG 958
Db 272 ThrThrLeuArgLysLeuValThrLeuAsnAspArgSerArgAsnIleLeuThrVal 291
QY 959 ATTGATCGAATAAAGACACCTAAACATATCTCATATTCGCTTACCCCTGGGGTGGG 1018
Db 292 GluAspProIleGluTyrLeuGlu-----GlyIleGly 303
QY 1019 AGAAGCTTGAAGTCTCAAGTCAAGTC---GTGGCCCTGTGCTGCTTGGGACAGC 1075
Db 304 GluThr-----GlnValAsnProArgValAspMetThrPheAlaArgGlyLeuArg 320
```


TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5218

Alignment Scores:

Pred. No.:	0.559	Length:	804
Score:	95.00	Matches:	72
Percent Similarity:	33.81%	Conservative:	69
Best Local Similarity:	17.27%	Mismatches:	128
Query Match:	3.41%	Indels:	148
DB:	4	Gaps:	16

US-09-745-506-74 (1-1553) x US-09-134-001C-5218 (1-804)

```

QY 266 TCCTCCTTGAATGACCTTGACATCCCTCGTTGCTGAGAGTGGACATGTTGATTA 325
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84 SerSerValTyrAsp---AlaMetValArgLeuSerGlnAspTrpLysLeuArgHleVal 102
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 326 CTGCTGGAA-----CCAGCCGACCATACCTGTAAT 358
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 103 LeuIleGluMetHisGlyAsnAsnGlySerIleAspAsnAspProProAlaAlaMetArg 122
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 359 ---ACACTCTTCTGACCAATGACCTGACATGAGAGATGAGAGAGTGTGCAAAAG 415
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 123 TyrThrGluAlaLysLeuSerGlnLeuSerGlnGluLeuLeuArgAspIleAsnLysGlu 142
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 416 AAGCAGACCTCATCTCTCTACCATCCGCTATCTTCGACCCATGAGAGCGCATTAAC 475
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 ThrValSerPheIleProAsnLysAspThrThrLeuGluPromet----- 158
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 476 TGGAAACATGGAAGAGCGCTGTGATCCGGCTCTGGAAGACAGTGGTATCTAC 535
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 159 -----ValLeuProAlaArgPheProAsnLeuLeuIleAsnGlySerThrGlyIleSer 176
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 536 TCT-----CCTCATACA----- 547
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 177 SerGlyTyrAlaThrAspIleProProHisAsnLeuAlaGluValIleGlnGlyThrLeu 196
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 548 GCGTATGATGCTGCCGCCAGGCGGTCAACAACATGCTGGTAAAGGCTTGAGACTTGT 607
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 197 LysTyrIleAspGlnProAspIleThrIleAsnGlnLeuMetLysTyrIle----- 213
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 608 AACTCCAGGCCCATATCATCTCCCAAGCTCCCACTACCTCCACAGAGGAAACCAACGA 667
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 214 -----LysGlyProAspPheProThrGlyGly----- 222
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 668 GTAGAATTCAACGTTACTACACCCAGACCTGAGCAAAATCATCTGCACTGAAGA 727
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 223 -----IleIleGlnGly 226
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 728 ATTGACGCTGTTCT----- 742
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 227 IleGlnGlyIleLysAlaLysIleValThrGlyLysGlyValValValArgSerArg 246
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 743 GTCACTTCTTTTTCGTAGACCTGTATAGAGAA-----CAAAACGGATTATCTG 796
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 247 ValAspGluGluProLeuArgSerGlyArgLysGlnLeuIleValThrGluIleProTyr 266
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 797 AATTGTACTAGAAAGCTTTGATGACAGTGTAGATTTCTTCCCGAACAACAACACT 856
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 GluValAsnLysSerSerLeuValLysArgIleAspGluLeuArgAlaAspLysLys--- 285
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 857 TATCAGAAAGCGAAATCTGTCACTGGAAGACCTTGTCTACATCTGGAATGGGA 916
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 285 ----- 285
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 917 CGGTATGACACTGTGAGATCTGTCTCCCTGGCAACCATGATGATGAATAAAGA 976
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 286 -----ValAspGlyIleValGluValArgAspGluThrAspArg----- 298
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 977 CACCTAAACATATTCGCTATGCGCTTGGGGTGGGAGAACCTTAGAGTCTCA 1036
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 299 -----ThrGlyLeuArgIleAlaIleGluLeuLysLysAspAlaAsnSer--- 313
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

QY 1037 GTCAAACTCGTGGCCCTGTGTGCTGTGTTTGAGGACAGCGTTCTGCAGGCTGTGACCT 1096
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 314 -----GluSerIleLysAsn 318
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1097 GACCTTACCTCACAGGTGAGATG-----TCCATCATGATACTTTGATGCTGTCC 1150
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 319 TyrLeuTyrIysAsnSerAspLeuGlnIleSerTyrAsnPheAsnMetValAlaIleSer 338
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1151 CAAAGAAATTAATGTCATCTCTGTGAACAGCAACACTGAACGAGGCTTTCTTGAC 1210
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 339 GluGly-----ArgProLysLeuMetGly 346
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1211 CTTCGAGATATGCTGATTCATCTCACTTGAGAGATAATATATATATATATATATATATAT 1270
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 347 LeuArgGluIleIleGluSerTyrLeuAsnHisGlnIleGluValAlaThrAsnArgThr 366
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1271 GACAGGACCCCTCTTCAGTGTGTAAATTCGAGAAACATCAGATTAACATTCCTACAA 1330
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 367 ArgTyrAsp-----LeuGluGlnAlaGluLysArgMetHisIleVal 380
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1331 ATCAGCTGAGATGCCCACTTAATTTGTACATGATGATGAGTGGAGCTGTG 1381
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 381 GluGlyLeuMetLysAlaLeuSerIleLeuAspGluValIleAlaLeuIle 397
    |||||::: ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Search completed: August 22, 2003, 14:07:00
Job time : 46 secs